Online-Only Abstracts: Population-based burden of bloodstream infections in Finland

Description and plasmid characterization of *qnrD* determinants in *Proteus mirabilis* and *Morganella morganii*

A. Mazzariol[1], B. Kocsis[1,2], R. Koncan[1], E. Kocsis[1], P. Lanzafame[3] and G. Cornaglia[1]

1) *Department of Pathology and Diagnostics, University of Verona, Verona, Italy,* 2) *Institute of Medical Microbiology, Semmelweis University, Budapest, Hungary and* 3) *Microbiologia e Virologia, Presidio Ospedaliero Santa Chiara, Trento, Italy*

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Abstract

We investigated the presence of *qnrC* and *qnrD* among 756 non-replicate *Enterobacteriaceae* isolated in Italy, selected for being non-susceptible to fluoroquinolones and/or resistant to third-generation cephalosporins. Four *Proteus mirabilis* and one *Morganella morganii* (0.66% of the total) presented a *qnrD* gene, located in a 2687-base-pair plasmid that was entirely sequenced. The plasmid is un-typable, and contains no known coding region other than *qnrD*. That the *qnrD* gene was found in four unrelated *P. mirabilis* and in one *M. morganii* isolate might suggest a frequent association of this gene with the tribe *Proteeae*.

Sequence Type ST131 and ST10 Complex (ST617) predominant among CTX-M-15-producing *Escherichia coli* isolates from Nigeria

I. Aibinu[1,2], T. Odugbemi[1], W. Koenig[2] and B. Ghebremedhin[2]

1) *Department of Medical Microbiology and Parasitology, University of Lagos, Lagos, Nigeria and* 2) *Institute of Medical Microbiology, OVGU, Magdeburg, Germany*

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Abstract

Of 109 clinical *Escherichia coli* isolates from two major tertiary hospitals in Lagos (University Teaching Hospital and the National Orthopaedic Hospital Igbobi), 14 (12.8%) extended-spectrum beta-lactamse (ESBL) producers were characterized using PCR and sequencing,

ERIC-PCR and multilocus sequence typing. All ESBL-producing isolates encoded only the CTX-M-15 gene. Clonal group ST131 (35.7%) was the predominant ST, followed by ST617 (28.6%). Isolated cases of other sequence types were also observed. Plasmid-mediated quinolone resistance genes *qnrA*, *qnrB1* and *aac-(6′)-Ib-cr* were detected among these ESBL isolates of different clonal groups. This is the first description of the clonality of CTX-M-15-producing *E. coli* from Nigeria. The presence of diverse clonal lineages shows the continuing potential for genetic diversification and emergence of new epidemic strains.

Prevalence of 16S rRNA methylase genes in Enterobacteriaceae isolates from a Greek University Hospital

I. Galani, M. Souli, T. Panagea, G. Poulakou, K. Kanellakopoulou and H. Giamarellou

4th Department of Internal Medicine, Infectious Disease Laboratory, Molecular Biology Section, Athens University School of Medicine, Chaidari, Greece

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Abstract

16S ribosomal RNA methylase-mediated high-level resistance to 4-,6-aminoglycosides has been reported in clinical isolates of gram-negative bacilli from several countries. Three of 1534 (0.2%) isolates of *Klebsiella pneumoniae* and three of 734 (0.4%) *Proteus mirabilis* isolates from a university hospital in Athens, Greece, were positive for *rmtB* and highly resistant to all aminoglycosides tested (MICs ≥256 mg/L). Two of the *K. pneumoniae rmtB*-bearing isolates, were KPC-2 and OXA-10 producers and the third was a DHA-1 producer. One of the *P. mirabilis* isolates was a VIM-1 and OXA-10 producer and one was an OXA-10 producer. All *rmtB*-harbouring isolates were clonally unrelated. None of the *E. coli* (n = 1398) and *Enterobacter* spp. (n = 414) isolates were positive for *armA*, *rmtA*, *rmtB*, *rmtC* or *rmtD*.